

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/980,364A
Source: 1FW16
Date Processed by STIC: 7/10/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 07/10/2006

PATENT APPLICATION: US/09/980,364A

TIME: 12:51:55

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\07102006\I980364A.raw

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3 <110> APPLICANT: Boutilier, Kim
4   Ouellet, Therese
5   Custers, Jan
6   Hattori, Jiro
7   Miki, Brian
8   Van Lookeren Campagne, Michiel
10 <120> TITLE OF INVENTION: USE OF THE BNM3 TRANSCRIPTIONAL ACTIVATOR TO CONTROL PLANT
11   EMBRYOGENESIS AND REGENERATION PROCESSES
13 <130> FILE REFERENCE: 15327.0001US01
15 <140> CURRENT APPLICATION NUMBER: 09/980,364A
16 <141> CURRENT FILING DATE: 2002-04-08
18 <150> PRIOR APPLICATION NUMBER: PCT/CA00/00642
19 <151> PRIOR FILING DATE: 2000-06-02
21 <150> PRIOR APPLICATION NUMBER: EP 99201745.9
22 <151> PRIOR FILING DATE: 1999-06-02
24 <160> NUMBER OF SEQ ID NOS: 17
26 <170> SOFTWARE: PatentIn version 3.3
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 2014
30 <212> TYPE: DNA
31 <213> ORGANISM: Brassica napus
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38 tgaataataa ctggttaggc ttttctctct ctcttatga acaaaatcac catcgtaagg      180
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42 cgaccgctgc ctccgatgag tcttcagcca tccaaacatc gtttcttctt ccttttggtg      300
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52 ggctgagaaa tcaaccctgt gataatggtg ataatacaaga aaatggcaat gctgcaaaag      600
54 gcctgtccct ctcaatgaac tcatctactt cttgtgataa caacaacgac agcaataaca      660
56 acgttggtgc ccaagggaag actattgatg atagcgttga agctacaccg aagaaaacta      720
58 ttgagagttt tggacagagg acgtctatat accgcggtgt tacaaggcat cgggtggacag      780
60 gaagatatga ggcacattta tgggataata gttgtaaaag agaaggccaa acgcgcaaag      840
62 gaagacaagt ttatttgga gggtatgaca aagaagaaaa agcagctagg gcttatgatt      900
64 tagccgcact caagtattgg ggaaccacca ctactactaa cttcccatg agcgaatatg      960
66 aaaaagaggt agaagagatg aagcacatga caaggcaaga gtatggtgcc tctactgcga      1020
68 ggaaaagtag tggtttctct cgtggtgcat cgatttatcg tggagtaaca agacatcacc      1080
70 aacatggaag atggcaagct aggataggaa gagtcgcccg taacaaagac ctctacttgg      1140
72 gaacttttgg cacacaagaa gaagctgcag aggcatacga cattgcggcc atcaaattca      1200
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90 gtgagtttga ttataacgca agaaaccatt attactttgc tcagcagcag cagaccagc 1740
92 agtcgccagg tggagatttt cccgcggcaa tgacgaataa tgttggtctt aatatgtatt 1800
94 accatgggga aggtgggtga gaagttgctc caacatttac agtttggaac gacaattaga 1860
96 aaaaatagtt aaagatcttt agttatatgc gttgttggtg gctggtgaac agtgtgatac 1920
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118 Val Ala Gly Glu Tyr Cys Tyr Asp Pro Thr Ala Ala Ser Asp Glu Ser
119 35 40 45
122 Ser Ala Ile Gln Thr Ser Phe Pro Ser Pro Phe Gly Val Val Val Asp
123 50 55 60
126 Ala Phe Thr Arg Asp Asn Asn Ser His Ser Arg Asp Trp Asp Ile Asn
127 65 70 75 80
130 Gly Cys Ala Cys Asn Asn Ile His Asn Asp Glu Gln Asp Gly Pro Lys
131 85 90 95
134 Leu Glu Asn Phe Leu Gly Arg Thr Thr Thr Ile Tyr Asn Thr Asn Glu
135 100 105 110
138 Asn Val Gly Asp Gly Ser Gly Ser Gly Cys Tyr Gly Gly Gly Asp Gly
139 115 120 125
142 Gly Gly Gly Ser Leu Gly Leu Ser Met Ile Lys Thr Trp Leu Arg Asn
143 130 135 140
146 Gln Pro Val Asp Asn Val Asp Asn Gln Glu Asn Gly Asn Ala Ala Lys
147 145 150 155 160
150 Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Cys Asp Asn Asn Asn
151 165 170 175
154 Asp Ser Asn Asn Asn Val Val Ala Gln Gly Lys Thr Ile Asp Asp Ser
155 180 185 190
158 Val Glu Ala Thr Pro Lys Lys Thr Ile Glu Ser Phe Gly Gln Arg Thr
159 195 200 205
162 Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
163 210 215 220
166 Ala His Leu Trp Asp Asn Ser Cys Lys Arg Glu Gly Gln Thr Arg Lys
167 225 230 235 240
170 Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala

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174 Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr
175          260          265          270
178 Thr Asn Phe Pro Met Ser Glu Tyr Glu Lys Glu Val Glu Glu Met Lys
179          275          280          285
182 His Met Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg Arg Lys Ser Ser
183          290          295          300
186 Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
187 305          310          315          320
190 Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
191          325          330          335
194 Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala
195          340          345          350
198 Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Thr Ala Val Thr Asn
199          355          360          365
202 Phe Asp Met Asn Arg Tyr Asn Val Lys Ala Ile Leu Glu Ser Pro Ser
203          370          375          380
206 Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala Asn Arg Pro
207 385          390          395          400
210 Val Pro Ser Met Met Met Ile Ser Asn Asn Val Ser Glu Ser Glu Asn
211          405          410          415
214 Ser Ala Ser Gly Trp Gln Asn Ala Ala Val Gln His His Gln Gly Val
215          420          425          430
218 Asp Leu Ser Leu Leu His Gln His Gln Glu Arg Tyr Asn Gly Tyr Tyr
219          435          440          445
222 Tyr Asn Gly Gly Asn Leu Ser Ser Glu Ser Ala Arg Ala Cys Phe Lys
223          450          455          460
226 Gln Glu Asp Asp Gln His His Phe Leu Ser Asn Thr Gln Ser Leu Met
227 465          470          475          480
230 Thr Asn Ile Asp His Gln Ser Ser Val Ser Asp Asp Ser Val Thr Val
231          485          490          495
234 Cys Gly Asn Val Val Gly Tyr Gly Gly Tyr Gln Gly Phe Ala Ala Pro
235          500          505          510
238 Val Asn Cys Asp Ala Tyr Ala Ala Ser Glu Phe Asp Tyr Asn Ala Arg
239          515          520          525
242 Asn His Tyr Tyr Phe Ala Gln Gln Gln Gln Thr Gln Gln Ser Pro Gly
243          530          535          540
246 Gly Asp Phe Pro Ala Ala Met Thr Asn Asn Val Gly Ser Asn Met Tyr
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258 <210> SEQ ID NO: 3
259 <211> LENGTH: 2011
260 <212> TYPE: DNA
261 <213> ORGANISM: Brassica napus
263 <400> SEQUENCE: 3
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272 atgctttcac cagagacaac aatagtcact cccgagattg ggacatcaat ggtagtgcac      300
274 gtaataacat ccacaatgat gagcaagatg gaccaaact tgagaatttc cttggccgca      360
276 ccaccacgat ttacaacacc aacgaaaacg ttggagatat cgatggaagt ggggtgttatg      420
278 gaggaggaga cgggtggtggt ggctcactag gactttcgat gataaagaca tggctgagaa      480
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282 tctcaatgaa ctcatctact tcttgtgata acaacaacta cagcagtaac aacctgttg      600
284 cccaagggaa gactattgat gatagcgttg aagctacacc gaagaaaact attgagagtt      660
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296 gtggtttctc tcgtggtgca tcgatttatc gtggagtaac aagacatcac caacatggaa     1020
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300 gcacacaaga agaagctgca gaggcatacg acattgcggc catcaaattc agaggattaa     1140
302 ccgcagtgac taacttcgac atgaacagat acaacgttaa agcaatcctc gaaagcccta     1200
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318 actataacgc aagaaacctat tattactttg ctacgcagca gcagaccag cattcgccag     1680
320 gaggagattt tccgcgaggca atgacgaata atgttggtc taatatgtat taccatgggg     1740
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324 taaagatctt tagttatatg cgttgtttg tgggtgttgaa cagtttgata ctttgattat     1860
326 gttttttttt ctctttttca ttttgtttg tagtttttta agacttattt tttgtttcca     1920
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333 <210> SEQ ID NO: 4

334 <211> LENGTH: 579

335 <212> TYPE: PRT

336 <213> ORGANISM: Brassica napus

338 <400> SEQUENCE: 4

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344 His His Arg Lys Asp Val Cys Ser Ser Thr Thr Thr Thr Ala Val Asp
345          20          25          30
348 Val Ala Gly Glu Tyr Cys Tyr Asp Pro Thr Ala Ala Ser Asp Glu Ser
349          35          40          45
352 Ser Ala Ile Gln Thr Ser Phe Pro Ser Pro Phe Gly Val Val Leu Asp
353          50          55          60
356 Ala Phe Thr Arg Asp Asn Asn Ser His Ser Arg Asp Trp Asp Ile Asn
357 65          70          75          80
360 Gly Ser Ala Cys Asn Asn Ile His Asn Asp Glu Gln Asp Gly Pro Lys
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372 Gly Gly Gly Ser Leu Gly Leu Ser Met Ile Lys Thr Trp Leu Arg Asn
373          130          135          140
376 Gln Pro Val Asp Asn Val Asp Asn Gln Glu Asn Gly Asn Gly Ala Lys
377 145          150          155          160
380 Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Cys Asp Asn Asn Asn
381          165          170          175
384 Tyr Ser Ser Asn Asn Leu Val Ala Gln Gly Lys Thr Ile Asp Asp Ser
385          180          185          190
388 Val Glu Ala Thr Pro Lys Lys Thr Ile Glu Ser Phe Gly Gln Arg Thr
389          195          200          205
392 Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
393          210          215          220
396 Ala His Leu Trp Asp Asn Ser Cys Lys Arg Glu Gly Gln Thr Arg Lys
397 225          230          235          240
400 Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala
401          245          250          255
404 Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr
405          260          265          270
408 Thr Asn Phe Pro Met Ser Glu Tyr Glu Lys Glu Ile Glu Glu Met Lys
409          275          280          285
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413          290          295          300
416 Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
417 305          310          315          320
420 Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
421          325          330          335
424 Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala
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428 Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Thr Ala Val Thr Asn
429          355          360          365
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433          370          375          380
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437 385          390          395          400
440 Val Pro Ser Met Met Met Ile Ser Asn Asn Val Ser Glu Ser Glu Asn
441          405          410          415
444 Asn Ala Ser Gly Trp Gln Asn Ala Ala Val Gln His His Gln Gly Val
445          420          425          430
448 Asp Leu Ser Leu Leu Gln Gln His Gln Glu Arg Tyr Asn Gly Tyr Tyr
449          435          440          445
452 Tyr Asn Gly Gly Asn Leu Ser Ser Glu Ser Ala Arg Ala Cys Phe Lys
453          450          455          460
456 Gln Glu Asp Asp Gln His His Phe Leu Ser Asn Thr Gln Ser Leu Met
457 465          470          475          480
460 Thr Asn Ile Asp His Gln Ser Ser Val Ser Asp Asp Ser Val Thr Val

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/10/2006
PATENT APPLICATION: US/09/980,364A TIME: 12:51:56

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\07102006\I980364A.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:8,9,10,11,12,13,14

VERIFICATION SUMMARY

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